

Re-run



PCT

RAW SEQUENCE LISTING

DATE: 05/08/2002

PATENT APPLICATION: US/09/868,605

TIME: 11:02:33

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1 <110> APPLICANT: ML Laboratories PLC
 2 <120> TITLE OF INVENTION: Immunosuppression
 3 <130> FILE REFERENCE: P15700WO
 4 <140> CURRENT APPLICATION NUMBER: US/09/868,605
 5 <141> CURRENT FILING DATE: 2001-06-19
 6 <150> PRIOR APPLICATION NUMBER: 9827921.9
 7 <151> PRIOR FILING DATE: 1998-12-19
 8 <150> PRIOR APPLICATION NUMBER: 9925015.1
 9 <151> PRIOR FILING DATE: 1999-10-23
 10 <160> NUMBER OF SEQ ID NOS: 39
 11 <170> SOFTWARE: PatentIn Ver. 2.1
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 14 <211> LENGTH: 288
 15 <212> TYPE: PRT
 16 <213> ORGANISM: Homo sapiens
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 21 20 25 30
 22 Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
 23 35 40 45
 24 Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
 25 50 55 60
 26 Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp
 27 65 70 75 80
 28 Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr
 29 85 90 95
 30 Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly
 31 100 105 110
 32 Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg
 33 115 120 125
 34 Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr
 35 130 135 140
 36 Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile
 37 145 150 155 160
 38 Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu
 39 165 170 175
 40 Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp
 41 180 185 190
 42 Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met
 43 195 200 205
 44 Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg

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47      225          230          235          240
48      Asp Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly
49          245          250          255
50      Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg
51          260          265          270
52      Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val
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62      aaccaaagcc tgagtgaagt agtagtattt tggcaggacc aggaaaactt gggtctgaat 180
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67      ataacagaaa atgtgtacat aaatttgacc tgctcatcta tacacgggta ccagaacct 480
68      aagaagatga gtgttttgct aagaaccaag aattcaacta tcgagtatga tgggtattatg 540
69      cagaaatctc aagataatgt cacagaactg tacgacgttt ccatcagctt gtctgtttca 600
70      ttccctgatg ttacgagcaa tatgaccatc ttctgtattc tggaaaactg caagacgcgg 660
71      cttttatctt cacctttctc tataagagctt gaggaccctc agcctcccc agaccacatt 720
72      ccttggatta cagctgtact tccaacagtt attatatgtg tgatggtttt ctgtctaatt 780
73      ctatggaaat ggaagaagaa gaagcggcct cgcaactctt ataaatgtgg aaccaacaca 840
74      atggagaggg aagagagtga acagaccaag aaaagagaaa aaatccatat acctgaaaga 900
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86          20          25          30
87      Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val
88          35          40          45
89      Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu
90          50          55          60
91      Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr
92          65          70          75          80
93      Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile
94          85          90          95
95      Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys Lys Pro Thr

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97  Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala
98          115          120          125
99  Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile Thr Glu Asn
100         130         135         140
101  Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr Pro Glu Pro
102         145         150         155         160
103  Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr Ile Glu Tyr
104          165          170          175
105  Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu Leu Tyr Asp
106          180          185          190
107  Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr Ser Asn Met
108          195          200          205
109  Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu Leu Ser Ser
110         210         215         220
111  Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro Asp His Ile
112        225        230        235        240
113  Pro Trp Ile Thr Ala Val Leu Pro Thr Val Ile Ile Cys Val Met Val
114          245          250          255
115  Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys Lys Lys Arg Pro Arg Asn
116          260          265          270
117  Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu Arg Glu Glu Ser Glu Gln
118          275          280          285
119  Thr Lys Lys Arg Glu Lys Ile His Ile Pro Glu Arg Ser Asp Glu Ala
120         290         295         300
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129 <400> SEQUENCE: 4
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131  gaaccaccca ctgcatgcag agaaaaacag tacctaataa acagtcagtg ctgttctttg 120
132  tgccagccag gacagaaact ggtgagtgac tgcacagagt tcactgaaac ggaatgcctt 180
133  ccttgcggtg aaagcgaatt cctagacacc tggaacagag agacacactg ccaccagcac 240
134  aaatactgcg accccaacct agggcttcgg gtccagcaga agggcacctc agaaacagac 300
135  accatctgca cctgtgaaga aggctggcac tgtacgagtg aggcctgtga gagctgtgtc 360
136  ctgcaccgct catgctcgcc cggttttggg gtcaagcaga ttgctacagg ggtttctgat 420
137  accatctgcg agccctgccc agtcggcttc ttctccaatg tgtcatctgc tttcgaaaaa 480
138  tgtcaccctt ggacaagctg tgagacaaa gacctgggtg tgcaacaggc aggcacaaac 540
139  aagactgatg ttgtctgttg tcccaggat cggctgagag ccctggtggt gatccccatc 600
140  atcttcggga tcctgttttg catcctcttg gtgctgggtc ttatcaaaaa ggtggccaag 660
141  aagccaacca ataaggcccc ccacccaag caggaacccc aggagatcaa ttttcccgac 720
142  gatcttctct gctccaacac tgctgtctca gtgcaggaga ctttacatgg atgccaaaccg 780
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145 <210> SEQ ID NO: 5
146 <211> LENGTH: 277

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154 Ile Asn Ser Gln Cys Cys Ser Leu Cys Gln Pro Gly Gln Lys Leu Val
155 35 40 45
156 Ser Asp Cys Thr Glu Phe Thr Glu Thr Glu Cys Leu Pro Cys Gly Glu
157 50 55 60
158 Ser Glu Phe Leu Asp Thr Trp Asn Arg Glu Thr His Cys His Gln His
159 65 70 75 80
160 Lys Tyr Cys Asp Pro Asn Leu Gly Leu Arg Val Gln Gln Lys Gly Thr
161 85 90 95
162 Ser Glu Thr Asp Thr Ile Cys Thr Cys Glu Glu Gly Trp His Cys Thr
163 100 105 110
164 Ser Glu Ala Cys Glu Ser Cys Val Leu His Arg Ser Cys Ser Pro Gly
165 115 120 125
166 Phe Gly Val Lys Gln Ile Ala Thr Gly Val Ser Asp Thr Ile Cys Glu
167 130 135 140
168 Pro Cys Pro Val Gly Phe Phe Ser Asn Val Ser Ser Ala Phe Glu Lys
169 145 150 155 160
170 Cys His Pro Trp Thr Ser Cys Glu Thr Lys Asp Leu Val Val Gln Gln
171 165 170 175
172 Ala Gly Thr Asn Lys Thr Asp Val Val Cys Gly Pro Gln Asp Arg Leu
173 180 185 190
174 Arg Ala Leu Val Val Ile Pro Ile Ile Phe Gly Ile Leu Phe Ala Ile
175 195 200 205
176 Leu Leu Val Leu Val Phe Ile Lys Lys Val Ala Lys Lys Pro Thr Asn
177 210 215 220
178 Lys Ala Pro His Pro Lys Gln Glu Pro Gln Glu Ile Asn Phe Pro Asp
179 225 230 235 240
180 Asp Leu Pro Gly Ser Asn Thr Ala Ala Pro Val Gln Glu Thr Leu His
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188 <211> LENGTH: 735
189 <212> TYPE: PRT
190 <213> ORGANISM: Homo sapiens
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195 20 25 30
196 Ala Gln Ile Gly Asp Ser Val Ser Leu Thr Cys Ser Thr Thr Gly Cys

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201		65				70					75					80			
202	Val	Ser	Phe	Gly	Asn	Glu	His	Ser	Tyr	Leu	Cys	Thr	Ala	Thr	Cys	Glu			
203					85					90					95				
204	Ser	Arg	Lys	Leu	Glu	Lys	Gly	Ile	Gln	Val	Glu	Ile	Tyr	Ser	Phe	Pro			
205				100					105					110					
206	Lys	Asp	Pro	Glu	Ile	His	Leu	Ser	Gly	Pro	Leu	Glu	Ala	Gly	Lys	Pro			
207			115					120					125						
208	Ile	Thr	Val	Lys	Cys	Ser	Val	Ala	Asp	Val	Tyr	Pro	Phe	Asp	Arg	Leu			
209		130					135					140							
210	Glu	Ile	Asp	Leu	Leu	Lys	Gly	Asp	His	Leu	Met	Lys	Ser	Gln	Glu	Phe			
211		145				150					155				160				
212	Leu	Glu	Asp	Ala	Asp	Arg	Lys	Ser	Leu	Glu	Thr	Lys	Ser	Leu	Glu	Val			
213					165					170					175				
214	Thr	Phe	Thr	Pro	Val	Ile	Glu	Asp	Ile	Gly	Lys	Val	Leu	Val	Cys	Arg			
215			180						185					190					
216	Ala	Lys	Leu	His	Ile	Asp	Glu	Met	Asp	Ser	Val	Pro	Thr	Val	Arg	Gln			
217		195						200					205						
218	Ala	Val	Lys	Glu	Leu	Gln	Val	Tyr	Ile	Ser	Pro	Lys	Asn	Thr	Val	Ile			
219		210				215						220							
220	Ser	Val	Asn	Pro	Ser	Thr	Lys	Leu	Gln	Glu	Gly	Gly	Ser	Val	Thr	Met			
221		225				230					235				240				
222	Thr	Cys	Ser	Ser	Glu	Gly	Leu	Pro	Ala	Pro	Glu	Ile	Phe	Trp	Ser	Lys			
223					245					250					255				
224	Lys	Leu	Asp	Asn	Gly	Asn	Leu	Gln	His	Leu	Ser	Gly	Asn	Ala	Thr	Leu			
225				260					265					270					
226	Thr	Leu	Ile	Ala	Met	Arg	Met	Glu	Asp	Ser	Gly	Ile	Tyr	Val	Cys	Glu			
227		275						280					285						
228	Gly	Val	Asn	Leu	Ile	Gly	Lys	Asn	Arg	Lys	Glu	Val	Glu	Leu	Ile	Val			
229		290				295						300							
230	Gln	Glu	Lys	Pro	Phe	Thr	Val	Glu	Ile	Ser	Pro	Gly	Pro	Arg	Ile	Ala			
231		305				310					315				320				
232	Ala	Gln	Ile	Gly	Asp	Ser	Val	Met	Leu	Thr	Cys	Ser	Val	Met	Gly	Cys			
233					325					330					335				
234	Glu	Ser	Pro	Ser	Phe	Ser	Trp	Arg	Thr	Gln	Ile	Asp	Ser	Pro	Leu	Ser			
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236	Gly	Lys	Val	Arg	Ser	Glu	Gly	Thr	Asn	Ser	Thr	Leu	Thr	Leu	Ser	Pro			
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238	Val	Ser	Phe	Glu	Asn	Glu	His	Ser	Tyr	Leu	Cys	Thr	Val	Thr	Cys	Gly			
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RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : N:\paola\US09868605.raw
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VERIFICATION SUMMARY

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